

**Table 2. Location and effect of QTL.**

Phenotypic class	Trait	Phenotypic mean of parental lines						LOD	PVE (%)	Phenotypic mean of genotypic classes			
		<i>M. zebra</i>		<i>L. fuelleborni</i>		QTL Name	Linkage Group	Map Position (cM)		MZ/MZ	MZ/LF	LF/LF	
		2	3	2	3								
DENTITION	LOWER JAW DENTITION	2	3	LJD 1	7	2.3	3.31**	7.2	2.5263	2.5367	2.7254		
				LJD 2	12	0	4.97**	12.8	2.4461	2.6473	2.8415		
				LJD 3	16	0	6.29**	18.4	2.4515	2.6289	2.8363		
	UPPER JAW DENTITION	2	3	UJD 1	7	2.3	3.43**	5.4	2.5449	2.5891	2.7549		
				UJD 2	12	0	4.52**	18.9	2.3746	2.6491	2.8841		
				UJD 3	16	0	5.28**	10.7	2.4963	2.6666	2.8321		
LOWER JAW LATERAL VIEW	LOWER JAW	-0.01092	0.117	LJL 1	1	68.8	10.54**	17.8	-0.0225	0.0000	0.0200		
				LJL 2	2	54.5	6.37**	11.4	-0.0094	-0.0036	0.0168		
				LJL 3	6	51.8	5.08**	8.7	-0.0077	0.0022	0.0146		
	DENTARY	0.0386	-0.0414	DNT 1	2	6	2.82*	6.8	0.0048	-0.0143	-0.0205		
				ART 1	2	64.1	2.65*	7.9	0.0102	-0.0109	-0.0248		
				ART 2	6	2	2.84*	6.3	0.0030	0.0003	-0.0190		
	ARTICULAR			ART 3	21	5	5.69**	14	0.0101	-0.0122	-0.0248		
		LOWER JAW LENGTH	0.8736	0.7633	JL 1	1	73.8	3.25*	9.2	0.8351	0.8289	0.8147	
				JL 2	2	59.5	4.02**	12	0.8352	0.8350	0.8141		
				JL 3	10	38.2	3.43**	7.4	0.8208	0.8154	0.8313		
	ARTICULAR ARM LENGTH	0.284	0.393	AAL 1	1	78.8	4.66**	11.8	0.3335	0.3389	0.3496		
				AAL 2	2	64.1	6.16**	15.8	0.3312	0.3420	0.3515		
				AAL 3	21	0	3.45**	6.5	0.3353	0.3463	0.3474		
LOWER JAW VENTRAL VIEW	LOWER JAW	-0.1531	0.1531	LJV 1	1	55.3	3.1*	6.6	-0.0405	-0.0204	-0.0152		
				LJV 2	11	28.9	3.66**	7.1	-0.0420	-0.0189	-0.0107		
				LJV 3	16	17.1	3.37**	9.4	-0.0441	-0.0172	-0.0154		
				LJV 4	25	9	4.5**	11.4	-0.0259	-0.0108	0.0121		
	LOWER JAW WIDTH	0.4361	0.7575	JW 1	1	55.3	3.86**	6.7	0.5239	0.5427	0.5502		
				JW 2	11	18.9	5.5**	13.2	0.5146	0.5424	0.5546		
				JW 3	14	3.6	3.5**	6.3	0.5239	0.5334	0.5502		
				JW 4	16	0	3.18*	8.7	0.5207	0.5474	0.5455		

				JW 5	20	0	3.09*	5.4	0.5272	0.5476	0.5470
				JW 6	25	9	4.67**	11.9	0.5405	0.5591	0.5758
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UPPER JAW	MAXILLA	-0.0743	0.0792	MX 1	2	78.9	3.54**	7.3	-0.0243	-0.0113	-0.0109
				MX 2	5	22.8	3.34*	7	-0.0249	-0.0125	-0.0102
				MX 3	9	35.9	2.75*	7.2	-0.0257	-0.0188	-0.0090
				MX 4	25	9	5.55**	14.6	-0.0116	-0.0048	0.0099
MAXILLARY PALATINAD WING LENGTH		0.2711	0.4407	PWL 1	9	35.9	3.84**	14.5	0.3239	0.3327	0.3507
				PWL 2	25	9	3.41**	9.1	0.3327	0.3369	0.3515
PREMAXILLA		0.1	-0.1077	PMX 1	2	39.2	2.92*	14.6	-0.0154	0.0048	-0.0204
				PMX 2	10	12.9	3.3**	9.5	-0.0024	-0.0128	0.0079
				PMX 3	16	48.2	3.78**	10.8	-0.0006	-0.0050	-0.0259
				PMX 4	26	1	2.7*	9.1	0.0396	-0.0031	-0.0356
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SUSPENSORY APPARATUS	SUSPENSORIUM	-0.0531	0.0531	SUS 1	4	34.2	2.83*	6.6	-0.0111	-0.0073	0.0028
				SUS 2	5	27.8	3.07*	7.6	-0.0133	0.0013	0.0003
				SUS 3	18	0	2.53*	7.9	-0.0133	-0.0025	0.0022
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SKULL	NEUROCRANIUM	-0.0449	0.0478	NCM 1	1	11.3	3.3**	11.8	-0.0083	0.0008	0.0064
				NCM 2	8	0	2.6*	9	0.0044	0.0076	-0.0047
VOMER		0.0514	-0.0514	VM 1	16	0	3.7**	18.6	0.0160	0.0048	-0.0085
				VM 2	24	8.5	3.1**	20.7	-0.0069	-0.0096	0.0145
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For each quantitative trait locus (QTL) detected the name, linkage group, map position (centiMorgans), likelihood of odds (LOD) score, percent variance explained (%), and effect are indicated. The phenotypic mean of *L. fuelleborni* and *M. zebra* is given as a reference. QTL were detected via MQM mapping. LOD thresholds were calculated via permutation test for each trait. Genome-wide significance levels were evaluated at the 95%\* and 99%\*\* levels.

of phenotypic values relative to *L. fuelleborni* and *M. zebra*.